USE OF MULTILINE CULTIVARS AND CULTIVAR MIXTURES FOR DISEASE MANAGEMENT

C. C. Mundt

Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331-2902; e-mail: mundtc@bcc.orst.edu

■ **Abstract** The usefulness of mixtures (multiline cultivars and cultivar mixtures) for disease management has been well demonstrated for rusts and powdery mildews of small grain crops. Such mixtures are more useful under some epidemiological conditions than under others, and experimental methodology, especially problems of scale, may be crucial in evaluating the potential efficacy of mixtures on disease. There are now examples of mixtures providing both low and high degrees of disease control for a wide range of pathosystems, including crops with large plants, and pathogens that demonstrate low host specificity, or are splash dispersed, soilborne, or insect vectored. Though most analyses of pathogen evolution in mixtures consider static costs of virulence to be the main mechanism countering selection for pathogen complexity, many other potential mechanisms need to be investigated. Agronomic and marketing considerations must be carefully evaluated when implementing mixture approaches to crop management. Practical difficulties associated with mixtures have often been overestimated, however, and mixtures will likely play an increasingly important role as we develop more sustainable agricultural systems.

INTRODUCTION

One of several crop diversification strategies for disease control (39, 40) is to grow mixtures of plants that differ in their reaction to a pathogen. The philosophy and concepts underlying the use of multiline cultivars (mixtures of lines bred for phenotypic uniformity of agronomic traits) and cultivar mixtures (mixtures of agronomically compatible cultivars with no additional breeding for phenotypic uniformity) were described elegantly in previous *Annual Review of Phytopathology* chapters (17, 167). Recent minireviews have summarized the epidemiological impacts of host diversity (45) and current research on cereal cultivar and species mixtures in Europe (36). Smithson & Lenne (153) have provided a thorough update of the literature on cultivar mixture effects on disease levels, yield, and yield stability for a range of crops. A website useful for teaching about mixtures in advanced plant pathology classes is now available (23).

381

A critical point that has previously been emphasized is that of functional diversity, i.e., disease reductions will not be obtained with all mixtures, and randomly chosen mixture components will not necessarily provide adequate disease control. Rather, mixture components need to be relevant, or functional, to the pathogen population in question (112, 147, 167). The effects of mixtures on disease intensity as compared to their component pure stands can range from a disease increase to nearly complete disease control (153). In this review, I discuss potential explanations for this large variation in mixture effects, both within and between pathosystems. I then discuss the effects of host diversity on pathogen evolution, and comment on considerations pertinent to implementation of diversity approaches in agricultural production. The term mixture is used to include both multiline cultivars and cultivar mixtures. Though intercropping (mixtures of different crop species) is important (14, 44), especially in traditional agriculture (157), that large and complex literature is not discussed here.

SPECIALIZED, FOLIAR PATHOGENS OF SMALL GRAINS

Most studies regarding the effects of host mixtures on disease have been with specialized, polycyclic, foliar pathogens of small grains, primarily rusts (*Puccinia* spp.) and powdery mildews (*Blumeria* [= *Erysiphe*] *graminis*), but there have been recent studies with rice (*Oryzae sativa*) blast, caused by *Magnaporthe grisea* (72, 103). These extensively grown, self-pollinated cereal crops have a long history of "boom-and-bust" cycles of effective control of disease followed by failure, as pathogens adapt to widely-deployed single race-specific resistance genes (13, 17, 68, 173). Host resistance is often the only economically viable control method for these diseases. Thus, strategies to increase resistance durability against these diseases have been of particular interest.

Several mechanisms have been postulated to explain the reduction in severity of disease caused by polycyclic, foliar pathogens that interact in a gene-for-gene manner with their hosts when mixtures are grown (17, 27, 45, 72, 112, 167). The dilution of inoculum that occurs due to increased distance between plants of the same genotype often appears to be the most important mechanism (20, 27, 167). However, other mechanisms may also be important (27, 72). For example, induced resistance, which is predicted to be important by simulation models (79), accounted for about 30% of the total reduction of yellow rust (caused by *Puccinia striiformis*) in wheat (*Triticum aestivum*) cultivar mixtures in the field (22). In another study with wheat yellow rust, cultivars resistant to all inoculated races compensated for susceptible cultivars through increased tiller number, and this compensation sometimes accounted for a very large percentage of the observed reduction in disease severity (37, 38). When each of the cultivars was susceptible to one or more races, however, this same effect was not seen (2). By comparing barley (*Hordeum vulgare*) cultivar mixtures containing either the same or different race-specific resistance genes, Wolfe et al. (170) estimated that differences in genetic background among cultivars contributed an additional 33% reduction of powdery

mildew beyond that provided by diversity for race-specific resistance. Though much is known about the efficacy of mixtures against foliar small grain diseases, there is still substantial variation in disease control attained in different studies. For example, powdery mildew of small grains is an ideal target for use of host mixtures, owing to a relative abundance of single-gene resistances, a small plant size, shallow dispersal gradient of the pathogen, and a large number of pathogen generations per crop season (45). Even in this case, however, there can be substantial variation in disease control among mixture studies. For example, Smithson & Lenne (153) noted disease reductions relative to pure stands ranging from 4% to 89%. Reasons for such large variation in the efficacy of mixtures on disease are discussed below.

Mixture Composition

For diversity to be functional, there must be an appropriate match between the resistance genes incorporated in a mixture and the avirulence genes present in the target pathogen population. Thus, a matrix of host and pathogen genotypes is usually considered, in an attempt to minimize the percentage of the host population toward which a given race will be virulent. Such information has been used to construct, and alter over time, the resistance genes utilized in multiline cultivars (18, 72). In the United Kingdom, tables have been provided to farmers in which small grain cultivars are placed into different diversification groups, based on their reactions to current virulence combinations of *P. striiformis* and *B. graminis* f. sp. *hordei* (142, 143). A similar process is almost always used in choosing resistance genotypes to include in mixtures, even if not in a formal way. Statistical approaches for choosing mixture components based on field analysis of two-way combinations of cultivars (71, 86) and of the local pathogen population (176) have been proposed. Molecular analyses of pathogen populations (177) and individual avirulence genes (82, 162) may provide further insights into the most appropriate resistance genes to deploy in host mixtures to maximize durability.

Given pathogen specificity, disease severity will decrease with decreasing frequency of a host genotype in mixture, as has been demonstrated numerous times with rusts and powdery mildews of small grains (17, 112, 167), and with rice blast (72, 103). Leonard's models (83) predict that the apparent infection rate (161) will decline logarithmically with the proportion of a genotype in mixture. This logarithmic relationship has been confirmed in the field for several small grain diseases (20, 33, 73, 83, 87, 88). Both logarithmic (36) and linear (2, 137) relationships have been reported between disease severity and host frequency.

Many experimental studies of mixtures have involved a single pathogen race and two host genotypes, with one host genotype being susceptible and the other completely resistant to that race. Such studies are useful to investigate the dilution effect of mixtures on disease, and are sometimes of practical use to protect an agronomically desirable but susceptible genotype by mixing it with a resistant, but less desirable, genotype (45). Most practical applications, however, involve a more complex matrix of host and pathogen genotypes, wherein each host genotype is susceptible to one or more pathogen races and each race may be virulent to more

than one host genotype. This allows for the use of resistance genes that have been "defeated," and for mechanisms such as induced resistance and interracial competition to function (112). In these differentially susceptible (45) mixtures, one would expect disease to decline with number of mixture components, if these components react differently to the pathogen genotypes in question. Though studied little, such a decline has been demonstrated in two cases (103, 122). However, these were average effects, and there is sufficient variation among specific mixtures such that a comparison of any two mixtures with differing number of genotypes may not demonstrate the expected result.

Given the logarithmic relationship between infection rate and host frequency described above, one would expect diminishing returns to decreasing frequency of a genotype in mixture or to an increase in the number of genotypes used in a mixture (83, 101). On the other hand, including a large number of genotypes in a mixture could be beneficial in slowing pathogen evolution toward complex virulence (91). In reality, practical considerations often play a large role. Genotypes included in a cultivar mixture usually must be agronomically competitive on their own, and mixing is usually done by farmers themselves or by seedsmen. Thus, the number of genotypes included in a cultivar mixture is usually very limited, often between two and four. The agronomic performance of genotypes included in a multiline cultivar is usually quite similar. In addition, individual lines are usually maintained by some type of certifying organization and provided to seed growers as a bulk population. As a consequence, as many as 8 to 12 lines have been included in some multiline cultivars (4, 18).

The slope of the relationship between a disease parameter (infection rate, % severity, etc.) and host frequency determines the strength of the mixture's effect on disease and will depend on several factors, including those discussed below.

Epidemic Intensity

Among the more important outcomes of Leonard's (83) model is that disease reduction due to mixing will increase with increasing generations of pathogen reproduction. For example, in an equal mixture of susceptible and immune plants, the predicted disease level on susceptible plants in the mixture relative to a pure stand of susceptible plants will be 0.5 in the first generation of secondary spread, 0.25 in the second generation, 0.125 in the third generation, etc. The number of pathogen generations that occur in a given epidemic will depend on the level of initial infection, the generation time of the pathogen, and the rate of epidemic development. The usual pattern seen in the field is for disease levels to initially diverge over time, as predicted by Leonard's (83) equations, and then to converge as the host's carrying capacity for disease is approached [for example, see (169)]. The reason for the convergence is that the absolute rate of disease increase eventually becomes lower in the pure stands than in the mixture as availability of uninfected host tissue in the more heavily infected pure stands limits epidemic progression (101).

Epidemic speed is also crucial. The more rapidly the host's carrying capacity for disease is approached, the less effective a mixture will be (101). For example, Alexander et al. (3) did not observe the level of stem rust (caused by *Puccinia graminis*) control they expected in wheat cultivar mixtures. Stem rust epidemics usually begin late in the growing season, the pathogen has a relatively long generation time, and rates of stem rust epidemics are often high. Based on Leonard's (83) exponential model, a disease reduction of 75% was expected (104) in Alexander et al.'s (3) plots, which consisted of 40% susceptible and 60% resistant plants. When logistic growth was assumed to account for the effects of limited carrying capacity, however, the predicted disease reduction was only 26% (104), a value very close to that observed in the field (3). The impact of carrying capacity may be even more extreme if one accounts for the important effect of latent infections on available infection sites (43). On the other hand, the rate of approach to carrying capacity may be much less significant if disease increase is discontinuous, as opposed to the continuous progression assumed by most analytical models of epidemic progression (45). Thus, divergence and subsequent convergence of disease levels in mixtures versus pure stands is likely to be the typical pattern seen in the field in a qualitative sense, but will differ quantitatively among pathosystems and environments.

As the major effect of mixtures is to reduce the infection efficiency of the pathogen through the dilution effect (see above), large amounts of external inoculum can greatly reduce the efficacy of a mixture for disease control. For example, year-round potato production in one region of Ecuador apparently resulted in large amounts of outside inoculum that masked the effect of potato (*Solanum tuberosum*) cultivar mixtures on late blight, caused by *Phytophthora infestans*. In contrast, mixture effects on late blight were greater at a site more distant from commercial potato production in Ecuador (48), and in more temperate areas of Peru (K.A. Garrett, L.N. Zuniga, E. Roncal, G.A. Forbes, C.C. Mundt & R.J. Nelson, in preparation) and the United States (47). A given level of outside inoculum will constitute a larger proportion of total inoculum in a mild epidemic than in a severe one (45), but the opposite could be true when conditions are favorable for epidemic development, and hence inoculum production, at a regional level.

The influence of epidemic intensity on mixture efficacy will thus depend on the underlying cause(s) of disease increase. If high disease incidence in pure stands is due to a fast approach to carrying capacity or large amounts of outside inoculum (either initially or on a continuing basis), then mixtures may be less effective in severe than in less severe epidemics. If, on the other hand, high disease incidence in pure stands is being driven by the number of pathogen generations, then mixtures may be more effective in severe than in less severe epidemics.

Spatial Scale

Disease control attained through host diversification can be influenced greatly by spatial scale of deployment, and it has been suggested that mixture efficacy

is greater in production-scale situations than in small-scale experimental plots
(103, 105, 167). There are several potential reasons for this spatial influence, three
of which are discussed below.

EXPERIMENTAL PROCEDURE AND DESIGN   Experimental plots are often artificially
inoculated, and at much higher concentrations than would be normal in nature, in an
attempt to assure disease establishment and to avoid stochastic effects in disease
establishment. This practice can reduce the number of generations of pathogen
increase that occur before the crop's carrying capacity for disease is reached, thus
reducing the effectiveness of mixtures on disease. A similar situation may arise
when infected "spreader plants" are placed within or around experimental plots
(9, 36), with the additional disadvantage of ongoing inoculum production from the
spreader plants throughout the epidemic.

Nearly all field experiments incorporate some type of "untreated" control, which
will have a greater severity of disease and produce greater amounts of inoculum
than other plots. In the case of mixtures, untreated controls are usually pure stands
of susceptible host genotypes. All types of disease control are affected by interplot
interference, including quantitative resistance (134) and fungicides (57). However,
mixture experiments are especially vulnerable to interplot interference because the
primary effect of mixtures, which is to reduce the pathogen's infection efficiency
through dilution of inoculum, can be overwhelmed by large amounts of outside
inoculum, as discussed above. In contrast, many fungicides and quantitative re-
sistance also impact the latent period, lesion expansion, and sporulation, which
are not directly affected by high concentrations of outside inoculation. The impor-
tance of interplot interference depends on factors such as the ratio of plot size to
area between plots, wind conditions, etc. (103, 135, 167). The mixture effect can
sometimes be obliterated by interplot interference (103, 167).

NATURE OF DISEASE SPREAD   Minogue & Fry (96) and van den Bosch et al. (159,
160) developed mathematical models that describe the movement of disease from a
focus as a traveling wave of constant velocity. Later, Ferrandino (34) suggested that
epidemic velocity will increase in time and space for wind-dispersed pathogens.
If disease spreads as a wave of constant velocity, then the difference in velocity
between a pure stand and a mixture will not be affected by the spatial scale of study.
If velocity increases in time and space, however, then the difference in velocity
between a pure stand and a mixture will become greater as disease expands in time
and space (105). Consequently, disease control will be relatively more effective
when studied over larger spatial scales. Through consideration of previous theo-
retical models (159, 160) and field studies with wheat yellow rust, van den Bosch
et al. (158) concluded, "In an ideal mixture of susceptible and resistant plants,
the radial velocity of focus expansion increases linearly with the logarithm of the
proportion of susceptible plants." This logarithmic relationship was confirmed in
a second study with wheat stripe rust (19) and a subsequent study with bean rust,
caused by *Uromyces appendiculatus* (5). It is not clear, however, whether velocities

were constant in these studies, as focus expansion was followed only until the radius reached 2 m or less. In contrast, recent studies with wheat stripe rust over greater distances (33 m) showed that epidemic velocity increases in time and space, and that this rate of change is greater for a pure stand than for a mixture (C.C. Mundt & L. Wallace, unpublished).

Many epidemics do not have a distinctly focal nature, and some may begin from numerous, randomly dispersed infections. Spatial scale may be of importance to the epidemiological results of diversity in these cases as well. It was earlier mentioned that mixtures are highly sensitive to the effect of external inoculum. Thus, mixtures with potentially functional diversity may not be as effective as desired in locations with substantial external inoculum. If, on the other hand, deployment of mixtures reduces inoculum densities on a regional basis, there may be a positive feedback, since less external inoculum may be experienced by any given field as mixtures are grown more extensively in the region (113).

OBSERVATION OF MIXTURES AT LARGE SPATIAL SCALE Comparisons of mixture performance at different spatial scales have usually been restricted to casual observations that mixtures provide better disease control at commercial scale than in small experimental plots (103, 167, 169) or that yield loss in mixtures has not been reported under extensive commercial use (18). Large-scale experiments with replicated treatments and appropriate controls are needed, but are prohibitively expensive and/or logistically impossible in most cases. There are, however, two examples in which careful evaluation of the commercial implementation of mixtures suggests that spatial scale may be of importance.

In the early 1980s, barley cultivar mixtures began to be used to control powdery mildew in the then German Democratic Republic, where the incidence of barley fields with severe mildew had reached about 50%. The percentage of fields sown to mixtures gradually increased to 92% (360,000 ha of mixtures) by 1990, while the incidence of severely infected fields declined to 10% and the percentage of fields sprayed with fungicide was reduced about threefold. Similar declines in barley powdery mildew were not observed over the same time period in adjacent countries, where diversification was not practiced (168, 171).

In a second example, in China, mixtures of glutinous rice cultivars highly susceptible to blast were mixed with non-glutinous cultivars that were more resistant, and compatible with a different set of blast races, than were the glutinous cultivars. Four mixtures were deployed in a total of 812 ha of contiguous rice fields spanning five townships in 1998 and in 3342 ha of contiguous rice fields over ten townships in 1999. A replicate of pure-line controls was planted in each township. Thus, mixtures were deployed in large, contiguous areas, but monoculture controls occupied a very small percentage of the total rice area, which minimized the effects of interference caused by high disease densities in pure stands. Mixtures reduced the severity of blast on susceptible glutinous rice cultivars by an average of 94% as compared to pure stands of the same cultivars (178). The practice expanded to 25,000 ha in 2000 and 100,000 ha in 2001 (Y. Zhu, personal communication).

Though results from the above two cases are encouraging, it is also important to keep in mind the "file drawer problem," i.e., positive results tend to become known, whereas negative results may be placed in a file drawer and never published (29b).

FACTORS DETERMINING MIXTURE IMPACTS ON OTHER PATHOSYSTEMS

Autoinfection/Alloinfection Ratio

Mixtures are unlikely to have significant effects on disease unless there is substantial exchange of inoculum among different host genotypes in the population. Thus, the effectiveness of mixtures for disease control is expected to decline with increasing proportion of autoinfection (8, 51, 120). Autoinfections are those "in which the donor (infector) host individual is the same as the recipient (infected) host individual," whereas alloinfections are those "in which the donor (or infector) host is a different individual from the recipient (or infected) host individual" (144). The proportion of autoinfection is influenced by both pathogen and host characteristics, as discussed below.

Dispersal

Steep inoculum dispersal gradients can result in high levels of autoinfection, and mathematical models have shown mixture efficacy to decline with increasing steepness of the pathogen's dispersal gradient (41, 68, 118, 174). There is some field evidence to support this contention. For example, bacterial pathogens are often splash dispersed, a process that can result in very steep dispersal gradients (42, 90). Mixture impacts less than those commonly recorded for rusts and powdery mildews of small grains have been observed for both bacterial blight of beans (*Phaseolus vulgaris*), caused by *Xanthomonas campestris* pv. *vesicatoria* (75), and bacterial blight of rice, caused by *Xanthomonas oryzae* pv. *oryzae* (1). Such observations do not isolate the effect of dispersal gradient steepness, however. For example, a small number of pathogen generations and substantial lesion expansion (see below) may reduce mixture effectiveness on bacterial blight of rice (1). In disease caused by splash-dispersed fungi, mixtures have also shown relatively low disease control (24, 50, 63, 93, 109, 115, 128, 150), though there are exceptions (60, 122). Comparisons are again confounded, as these splash-dispersed pathogens also tend to demonstrate less host specificity than is commonly seen with rusts and powdery mildews, and some of the results were from crops with plants larger than that of small grains.

Lesion Expansion

Continued expansion of an infection can contribute substantially to autoinfection, and is also a major contributor to total epidemic development (11). Computer simulations suggest that extensive lesion expansion can greatly reduce the efficacy

of mixtures on disease (77, 78). Studies in which environmental conditions and pathogen generation time were held constant showed that disease reductions in wheat mixtures were about twice as large for leaf rust (which has small, determinate lesions) as for wheat yellow rust (which demonstrates substantial lesion expansion) (77). In the field, approximately equal reductions of yellow rust and leaf rust were found in the same wheat cultivar mixtures (103). These mixtures were not designed for protection against leaf rust, however, and diversity may have been more functional against yellow rust than leaf rust, thus biasing the comparison.

Host Geometry

All else constant, autoinfection would be expected to increase with increasing genotype unit area (GUA), i.e., the ground area occupied by an independent, genetically homogeneous unit of host tissue (111). In a random mixture of host genotypes, the genotype unit is a plant, and GUA is the ground area occupied by an individual plant. Similarly, if host genotypes are instead deployed in alternating rows or in different fields, then GUA is the area occupied by a row and field, respectively. GUA does not account for intermingling of adjacent plants or three-dimensional dispersal of inoculum. It can, however, provide a useful approximation of the degree of mixing, or the "grain" of diversity sensu Pielou (138). Computer simulations and field studies showed that mixture efficacy decreases when the degree of aggregation of plant genotypes is changed to alter GUA (111, 117–120, 174). On average, rice mixtures controlled blast somewhat more effectively when plants were mixed within, rather than between, hills (72, 103) or rows (72). Random mixtures of sorghum (*Sorghum bicolor*) cultivars provided better control of *Colletotrichum sublineolum* and *Exserohilum turcicum* than did alternating rows of the same two cultivars (129). Similar results were found with yellow rust of wheat (16). As noted above, row mixtures of different rice cultivars were highly effective at controlling blast in China (178). It was impractical to include a comparison with random mixtures in that study, however.

GUA interacts with other spatial variables to determine disease severity in mixtures. Computer simulations (120) and field studies with rust pathogens (111, 117, 119) showed that GUA had little influence on mixture efficacy if initial inoculum was distributed in a single focus, rather than uniformly over plots. Later theoretical work suggested that the number of host units may be more important than their size, and that mixtures of large genotype units can provide substantial disease control, even when inoculum is distributed uniformly, provided that the total number of host units is sufficiently large (107). This is a difficult concept to test in the field, and results may be affected by shape and spatial pattern of genotype units, as well as by environmental conditions such as wind speed (108).

Overall, there is substantial variation in reported levels of disease control by mixtures for crops with plants larger than small grain cereals (7, 24, 75, 89, 92, 97, 119, 128, 129, 152, 156, 166). This is perhaps not surprising, given the large number of host and pathogen variables among the diseases represented. Nonetheless, there is an indication that mixtures may sometimes be of great value for controlling

diseases of crops with large plants, even for tree species. Computer simulations suggest that mixtures of apple (*Malus × domestica*) genotypes could reduce the severity of scab (caused by *Venturia inequalis*) from 86% to 34% (12). Preliminary field results showed 59% to 95% reductions of scab incidence on the cultivar Golden Delicious when grown in alternating rows with two other cultivars, though mixtures alone were not sufficient to provide commercially acceptable levels of control (89). In some cases, divergent results have been reported for highly similar pathosystems. For example, rust caused by *Melampsora* spp. was reduced by 50% or greater in mixtures of willow (*Salix* spp.) clones (92). In contrast, mixtures of poplar (*Populus* spp.) clones reduced infections of *Melampsora larici-populina* by 10% or less throughout most of the growing season (97). Conflicting results between the two *Melampsora* studies may have resulted from differences in effectiveness of the specific resistance genes deployed in each study or by differing experimental designs and procedures. In the case of the willow rust study (92), mixtures consisted of 5–6 clones, minimum plot size was 0.5 ha, and inoculation was natural. For poplar rust, the mixture was of three clones, plot size was only $2.8 × 3$ m, and epidemics were initiated with high levels of inoculum (97). Multiline cultivars of coffee (*Arabica* spp.) are used for protection against coffee rust (caused by *Hemileia vastatrix*) on 350,000 ha in Colombia (36, 98). This is a proactive program to protect the crop before the disease arrives and, thus, the epidemiological effects cannot be evaluated at this time.

It has been hypothesized that mixture effects on disease will be greater at high planting densities, owing to decreased plant size and, hence, decreased autoinfection (10). The influence of plant density on disease levels in pure stands must also be accounted for, however. Though it often is expected that disease severity will increase with plant density, field results are highly variable (14, 21). For example, the severity of barley powdery mildew declined with increased plant density, perhaps due to the decreased nutritional status of plants at high density (35). Thus, to isolate the effect of plant density on mixture efficacy for disease control, one needs to include all pure stands and all mixtures at a range of densities, a procedure that is often difficult to accomplish in the field (35). To my knowledge, this has been done in only one study. The effect of wheat cultivar mixtures on yellow rust severity was greatest at an intermediate planting density in two years, despite the fact that rust severity in pure stands increased with planting density in one year and decreased with planting density in the other year of the study (46).

Degree of Host-Pathogen Specificity

There are two situations in which the influence of host-pathogen specificity is relevant to mixtures. The first is for mixtures of host genotypes with partial resistance against pathogens that can also express a high degree of specificity, e.g., rusts and powdery mildews. The second situation is for host-pathogen systems that, as a whole, do not display the high degree of specificity typical of obligate parasites. For example, *Rhynchosporium secalis*, the causal agent of barley scald, can demonstrate host specificity (93), but this specificity is less stringent than for

biotrophic fungi and there are fewer sources of specific resistance available (122). In either situation, we are usually concerned with quantitative differences among host genotypes in mixture.

One approach to predict the epidemiological effect of such mixtures is to consider resistance to be qualitatively no different from specific resistance, and to simply account for the difference in resistance level between mixture components (45). Other more mechanistic approaches (51, 52, 59) account for differences in resistance components (e.g., infection frequency, latent period, and sporulation) between host components. These models predict that mixtures of partially resistant host genotypes can decrease, increase, or have no effect on disease severity relative to their component pure stands, depending on the relative levels of resistance components between host genotypes. Given that most pathosystems demonstrate some degree of specificity, quantitative adaptation of the pathogen to the differing host genetic backgrounds in mixtures (26, 76, 114, 170) could also lead to disease reductions in mixtures (26, 114).

Models that predict variability in performance among mixtures of host genotypes with partial resistance seem to better match field results. In the field, responses ranging from disease decreases to disease increases have been reported among mixtures of partially resistant genotypes for barley powdery mildew (124), barley scald (93), and Septoria tritici blotch of wheat (29a, 109; C. Cowger & C.C. Mundt, in preparation). In all of these studies, there were mixtures that showed disease increases in one year and disease decreases in another, perhaps owing to interactions of resistance components with environment. Averaged over all mixtures investigated, the majority of studies of mixtures of partially resistant host genotypes have shown relatively low levels of disease control (32, 50, 56, 63, 93, 109, 115, 124) or disease increases (125), though some have demonstrated reductions in disease similar to that expected with race-specific resistance and obligate parasites (60, 122, 150).

Diseases Caused by Viruses

There have been very few studies regarding the effects of mixtures on diseases caused by viruses. The outcome of mixtures on such diseases may be complicated by effects on vector abundance and behavior, as influenced by interactions with the transmission mode of the pathogen (140). Power (141) found that a 1:1 mixture of susceptible:resistant oat (*Avena sativa*) cultivars reduced the incidence of yellow dwarf to approximately the level observed in the resistant component for all three years of the study. In a different study of yellow dwarf, oat cultivar mixtures reduced disease incidence below the mean of the component pure stands for populations including two moderately resistant cultivars, but not in mixtures containing a highly susceptible and a moderately resistant cultivar (64).

Reductions of yellow dwarf incidence in the oat cultivar mixtures in Power's (141) study may have been caused by an interaction between vector behavior and virus transmission. Aphids in cultivar mixtures showed higher movement rates and shorter tenure times than aphids in pure stands. This may have reduced transmission

rates for this virus, because an aphid must feed for several hours to inoculate a host plant (141). The transmission dynamics of other pathogens could provide very different results. For example, maize (*Zea mays*) grown in association with beans greatly reduced the density of the leafhopper vector of the corn stunt spiroplasma, but not incidence of the disease. In this case, increased movement and decreased tenure times may have raised the number of transmissions per leafhopper, as the pathogen can be transmitted after very short feeding times by its vector (139).

The incidence of wheat soilborne mosaic was reduced by 33.2 and 39.8%, respectively, in 1:1 and 1:3 mixtures of susceptible:resistant cultivars. Further, the ELISA index of infected plants was 27.1% and 33.7% less in the 1:1 and 1:3 mixtures, respectively. Under field conditions, the resistant cultivar did not produce viruliferous zoospores of the soilborne vector, *Polymyxa graminis* (54). Thus, presence of the resistant cultivar in the mixture may have reduced virus transmission between susceptible plants in the mixture.

Soilborne Pathogens

The impact of mixtures on soilborne pathogens is likely to be determined by the extent to which secondary cycles of the pathogen occur, degree of host specificity, and spatial pattern of the pathogen in soil. As noted above, mixtures had a significant effect on wheat soilborne mosaic, a viral disease with a soilborne, protist vector (54). Mixtures of a resistant and a susceptible oat isoline decreased the disease index of Victoria blight and spore production of *Helminthosporium victoriae* in both field and greenhouse soil infested in foci (6). Crown and root rot of sugar beet (*Beta vulgaris*) caused by *Rhizoctonia solani* was reduced by mixing a susceptible cultivar with a highly resistant, but lower-yielding cultivar. Mixtures containing between 1/6 to 1/3 of the resistant cultivar provided yields superior to that of the susceptible cultivar in the presence of disease and yielded comparably to the susceptible cultivar in the absence of disease. This practice is now being rapidly adopted by sugar beet growers in Michigan (53; J.M. Halloin, personal communication). There are three published reports from different localities involving eyespot of wheat, caused by *Pseudocercosporella herpotrichoides*. All three studies included one or more mixtures of a cultivar possessing a major gene for resistance to *P. herpotrichoides* mixed with a susceptible cultivar. Results ranged from a statistically significant 13% reduction of eyespot severity (110) to smaller effects that were nonsignificant (109, 110, 146). Cultivar mixtures did not significantly reduce severity of eyespot in barley (50).

Interactions between plant genotypes in mixtures can sometimes provide yield benefits in the presence of soilborne pathogens, even when disease levels are not affected. The yield of mixtures of resistant and susceptible soybean (*Glycine max*) isolines at four of six locations was equal to that of the resistant pure stands in the presence of *Phytophthora sojae* because resistant isolines compensated for yield reductions as high as 35% experienced by susceptible isolines in mixture; substantial, though not complete, compensation occurred at the other two locations (165). Large yield increases over component means have often been recorded in

on-farm trials for wheat cultivar mixtures grown in the presence of *Cephalosporium gramineum*, despite the lack of an effect of mixtures on severity of Cephalosporium stripe disease (106, 116). This result was likely not due to simple compensation, however, as mixtures with the largest increases in yield were sometimes those consisting of cultivars with similar levels of resistance to Cephalosporium stripe. Averaged over three seasons, one wheat cultivar mixture yielded 9.1% greater than the mean of its component pure stands when inoculated with *P. herpotrichoides*, despite no effect on eyespot severity; the mean yield increase of this mixture in noninoculated plots was only 2.9% (110).

PATHOGEN EVOLUTION IN MIXTURES

As discussed above, race-specific resistance genes can continue to provide large epidemiological repercussions when deployed in mixtures, even after the matching virulence has evolved in the pathogen population. Will diversification also slow evolution to matching virulence of a given resistance gene? There are two issues to be considered. The first and simpler one is whether a given resistance gene will be more durable when deployed in a mixture than in a monoculture. A resistance gene deployed in a mixture will have less exposure to the pathogen population than if the same gene were deployed in monoculture of the same total crop area. This would be expected to reduce selection pressure and increase durability of that gene; limited field observations seem to support this view (103).

A more difficult question is whether a given number of resistance genes will be more durable if deployed in a mixture as compared to the same number of genes deployed sequentially in monoculture or combined into a single host genotype. Not surprisingly, mixtures support more diverse pathogen populations than do pure stands (18, 30, 72, 100), and the degree of diversity maintained within mixtures appears to be positively related to the degree of disease control provided (30). In the longer term, the question is whether mixtures will select for increased frequency of complex races, i.e., those with virulence corresponding to more than one resistance gene in the mixture. Unfortunately, this question is extremely difficult to test experimentally, and may require large areas and/or large amounts of time to address adequately.

In small-scale experimental plots, the relative frequency of complex *B. graminis* genotypes was greater in barley cultivar mixtures than in pure stand controls (26, 55, 121). Huang et al. (55) found that selection for complexity was less intense in row mixtures than in random mixtures of barley cultivars, supporting mathematical models (8, 51, 132) that predict less intense selection for complexity as autoinfection increases. At a larger spatial scale, the fungus increased in complexity in the former German Democratic Republic, where barley mixtures were being grown on as much as 360,000 ha. However, the same trend occurred in the former Czechoslovakia, where mixtures were not grown (171). Thus, it has been suggested that this increased complexity was an effect of migration, rather than selection by the mixtures (172).

It is more difficult to determine the selective influence of mixtures for clonal pathogens because virulence genes will not be randomly associated with other genes that influence pathogen fitness. In artificially inoculated plots, the proportion of complex races present in a mixture depended on the environment, host genotypes included in the mixture, and the genetic background of the complex race (30). In a very carefully designed greenhouse experiment, Kolmer (74) attempted to dissociate genetic background from virulence by first passing a population of *Puccinia graminis* through the sexual stage. Populations of the pathogen were then cycled on three different wheat multilines over 12 generations. He found strong selection for pathogen genotypes with virulence corresponding to three of the five resistance genes present in the multiline populations, but genotypes with four or five corresponding virulences represented a small minority and occurred at frequencies lower than predicted by a mathematical model. Given that the same virulences were selected on the susceptible, recurrent parent, this selection may have been due more to fitness effects associated with specific combinations of virulences than to any selective effect of the multilines. Thus, even in a well-designed experiment, it can be very difficult to make generalizations concerning the effects of mixtures on evolution of clonal pathogens.

Chin & Wolfe (26) have demonstrated that the manner in which genotype frequency data are expressed can strongly influence interpretation of evolutionary trends in mixtures. They found that the greater relative frequency of complex *B. graminis* genotypes in barley cultivar mixtures was attributable to the mixtures being highly effective in reducing the absolute frequency (number of colonies per tiller) of simple genotypes. In fact, the absolute frequency of the most complex genotype was less in a mixture of three barley cultivars than in the component pure stands, perhaps owing to the selective influence of different host genetic backgrounds in the mixtures (see below). After several years of extensive commercial use of barley cultivar mixtures in eastern Germany, there was an increase in the relative, but not absolute, frequency of *B. graminis* genotypes combining virulence to two of the three resistance genes most commonly used in the mixtures. Combining disease control and race frequency data in the wheat yellow rust study described above (30) also indicates a reduced absolute frequency of complex races in mixture as compared to pure stand, though data from only one susceptible pure stand was included in that study. It is thus possible that little loss of disease control would occur, despite an increase in relative frequency of complex pathogen genotypes in mixtures. For example, inoculation of an oat multiline with a race of *Puccinia coronata* virulent against all six resistance genes did not diminish the ability of the mixture to reduce disease severity (29 cited in 17). These results are all consistent with observations of natural ecosystems, in which complex races are the most frequent but do not displace all other genotypes (31, 148) and are not sufficiently fit to cause high levels of disease (148, 149). Selection for increased fitness of complex races could occur over multiple seasons in agricultural systems, if a mixture with a small number of host components were to be grown continuously (26).

The difficulty of studying pathogen evolution experimentally has encouraged the use of mathematical models. Earlier modeling studies of pathogen evolution

in mixtures have been summarized (67, 84, 91), and there have been additional contributions subsequently (51, 52, 80, 81, 151, 154, 175). Most of these models incorporate the status quo view on this topic, which assumes that fitness costs associated with virulence (more properly in most cases, a lack of avirulence) is the only mechanism to counter selection for increased virulence complexity in the pathogen. The advantage to a complex race of being able to attack multiple host genotypes in a mixture is hypothesized to be countered by a reduction in fitness associated with lack of avirulence genes that correspond to the matching resistance genes. In general, these models suggest that it will be difficult to prevent complex races from eventually dominating the pathogen population, though the process may be sufficiently slow such that the pathogen population can be managed.

Though models of pathogen evolution usually require a cost of virulence, evidence supporting such costs is very weak. Parlevliet (133) provided a thorough review of the literature regarding the cost-of-virulence concept, and found no association of virulence with fitness as a general phenomenon. More recent molecular analyses indicate that some avirulence genes can contribute to fitness pleiotropically, and that inactivation of such avirulence genes can lead to reduced pathogen fitness. This does not appear to be the general case, however, and "a majority of the known fungal avirulence genes have no obvious fitness function." Further, redundancy of avirulence genes in plant pathogens may allow pathogens to avoid resistance gene recognition, while retaining fitness functions associated with avirulence (82).

Parlevliet (133) explained the general lack of association between virulence and fitness in a two-step model consisting of mutation to virulence, which is often associated with a fitness reduction initially, followed by selection for fitness modifiers that eventually ameliorate the initial fitness cost. He supported this model with empirical observations from several pathosystems. Though largely ignored in plant pathology, such fitness modifiers play a critical role in evolutionary processes of other organisms. For example, selection for modifying genes can eliminate fitness reductions initially associated with antibiotic resistance in bacteria (28, 85, 99). Thus, selection for virulence in mixtures is likely to be more complex than is accounted for by static fitness costs, and selection for fitness modifiers is likely to be slower than selection for the virulence genes themselves (169). Further, it may be important to estimate initial fitness costs associated with virulence before there has been substantial selection for fitness modifiers.

Equally important to evaluating potential virulence costs is a need to examine other mechanisms (81, 84, 102, 112) that may counter selection towards increased pathogen complexity in mixtures. A few examples of such mechanisms are discussed below.

Alternative Mechanisms

Quantitative adaptation of pathogens to differing host genetic backgrounds present in crop mixtures could play a very important role in suppressing selection for complex races. For example, *B. graminis* isolates able to attack two different major

resistance genes were collected from pure stands of barley and barley cultivar mixtures containing these two resistances. Bulk populations of these isolates were then tested for infection efficiency on these same two host genotypes in the greenhouse. Populations derived from pure stands of the cultivar Hassan had a higher infection efficiency on Hassan than on the cultivar Wing, and vice versa. Populations derived from a mixture containing both Hassan and Wing had reduced infection efficiency on both cultivars, suggesting that a form of disruptive selection prevented this complex race from obtaining high fitness on both host components in the mixture (26). A similar result has recently been reported for *Blumeria graminis* f. sp. *tritici* (163) and *Mycosphaerella graminicola* (114) on wheat, though subsequent research did not demonstrate a consistent effect for *M. graminicola* (29a). Modeling studies suggest that differential adaptation to mixture components can greatly slow selection for a complex pathotype (81), and that the rate of selection for complexity is slowed by increased genetic diversity for fitness of the pathogen and by increasing rates of autoinfection (76).

It is usually assumed that the relative fitness of competing pathogen genotypes will be constant with regard to both population density and genotype frequency. However, differences in fitness components and effects of competition on these components can result in relative fitness being dependent on density and/or frequency (126, 127). In fact, modeling results indicate that relative fitness of competing pathogen genotypes will rarely be constant in nature (127). As pathogen density and genotype frequency change during the course of an epidemic, relative fitness may change over time, perhaps even reversing the fitness ranking of simple versus complex genotypes. Though experimental data are few, examples exist of both density-dependent (62, 65, 126, 130) and frequency-dependent (65, 126) selection for competing genotypes of plant pathogens. Simulation modeling suggests that density-dependent effects can slow selection for complex races in host mixtures, though density-dependence did not prevent the complex genotype from eventually dominating the simulated pathogen populations (80, 81).

Plant pathogen populations commonly undergo severe genetic bottlenecks, e.g., during overseasoning, and pathogen genotypes at low frequency may easily be lost owing to random drift during such times. Kiyosawa (67) suggested that genetic drift during overseasoning could be critically important to the rate of "breakdown" of resistant cultivars, and modeling results suggest that fungicide-resistant mutants can be lost through such random effects (95). Pathogen genotypes combining complex virulence with high fitness are likely to be in very low proportion initially. Thus, selection of highly fit, complex genotypes in mixtures could be greatly slowed through stochastic effects when population size is small. To my knowledge, all models of pathogen evolution in mixtures are deterministic, and thus do not account for the effect of genetic bottlenecks.

Selection for complex pathogen genotypes will be reduced if a large proportion of the initial inoculum consists of migrants from another area where mixtures are not grown. For example, immigration has a very large impact on the population genetics of *B. graminis* on small grains in Europe (171), and may have contributed

to the lack of strong selection for complex genotypes in barley cultivar mixtures grown in the former German Democratic Republic (172). The importance of migration will decline if similar mixtures are widely used, as a larger proportion of immigrants will have been exposed to the same selective pressure.

Selection in heterogeneous environments, a result of genotype × environment interaction, may slow selection for complex pathogen genotypes in mixtures. For example, race frequencies of *P. striiformis* were monitored in five three-way wheat cultivar mixtures planted at two locations and in two years (30). Complex races able to attack two of three mixture components often dominated in one location or year but not another. In no case did a complex race dominate in both years and locations in which the study was conducted. For powdery mildew of barley, on the other hand, the selective effect of cultivar mixtures on pathogen complexity showed substantial consistency between seasons (26, 55), perhaps because sexual reproduction distributed virulence genes randomly among multiple genetic backgrounds of the pathogen.

There will unquestionably be some selection toward increased relative frequency of complex races in host mixtures. After several decades of study, however, we still do not know the rate at which such selection will occur or to what degree, if any, it would decrease the disease control provided by mixtures. Answers should emerge from increased field experimentation and increased commercial use of mixtures. From a mechanistic standpoint, we need to abandon the old view of static costs of virulence being the primary mechanism to counter selection for increased pathogen complexity in mixtures. Other processes such as selection for fitness modifiers, disruptive selection, random drift, density- and/or frequency-dependent selection, genotype × environment interaction, or some combination of these factors will likely need to be accounted for.

Pathogen evolution can be managed to some extent by ensuring that no single mixture is grown exclusively in either time or space (169). Though such management can be done purposefully [for example, see (18)], it will occur as a matter of course in many cases. For example, new genotypes can easily be added to cultivar mixtures as agronomically superior cultivars are released. In Oregon, wheat growers purchase or mix seed of new wheat mixtures containing recently released cultivars; some growers simply blend a new cultivar into the mixture that they had previously been growing (103; C.C. Mundt, unpublished). Spatial diversity of mixtures is also likely to occur naturally, as different mixtures will perform better in different localities within a region, owing to differences in soil, climate, and management practices. In the former German Democratic Republic, eight barley cultivar mixtures incorporating 19 cultivars were utilized (171). In Washington state, 18% of the common soft white winter wheat area was sown to cultivar mixtures in autumn 2000 (total of 106,000 ha of mixtures), and this included at least 16 different mixtures (164). Even for perennial plantings, such as orchards, it may be possible to utilize different mixtures in time and space, since new plantings are continually being established over time, sometimes even within the same orchard.

IMPLEMENTATION

Mixtures are being used increasingly in commercial production around the world (36). Many of the initial studies and applications of mixtures in "modern" agriculture were multiline cultivars (112). Multiline cultivars are still being used today, and may be especially useful when a strongly favored agronomic parent is available or when crop uniformity is deemed crucial [for example, see (72, 98)]. In general, however, there has been a move in favor of cultivar mixtures over multilines. Cultivar mixtures are advantageous because they require no additional breeding effort and allow incorporation of agronomically superior cultivars as they become available. Further, increased genetic diversity among components of a cultivar mixture may provide additional control against the target disease, as well as some protection from nontarget diseases and abiotic stresses (169, 170). Though much of the work on mixtures has involved self-pollinated crops, recent work with pearl millet (*Pennisetum glaucum*) showed rust reductions and yield increases for mixtures of inbred lines, and especially for random-mated populations and mixtures of two- and three-way crosses (156). Wilson et al. (166) recently demonstrated a "dynamic multiline" approach in pearl millet that combines the advantages of both multilines and gene pyramids. Selection over four cycles of open pollination resulted in hybrid populations that reduced rust severity by 12–13% per cycle, and increased digestible biomass yield by 4.1% per generation. Such an approach also allows for selection of plant genotypes that have coevolved in a mixed population, which may contribute to improved performance of mixtures. In fact, arguments have been made in favor of selecting plant genotypes for their ability to perform well in mixtures for both self- and cross-pollinated species (39). Further research is needed to determine the costs and benefits in taking such an approach.

A useful mixture must provide yield benefits as well as disease control. Yield increases of 1–5% are often provided by cultivar mixtures in the absence of substantial disease, with larger increases when disease is of significance [for examples, see (38, 153, 169)]. Yield benefits can sometimes be substantially greater in large than in small plots (49, 169; C.C. Mundt, unpublished), often for unknown reasons beyond that of disease control attained in plots of different size (49; C.C. Mundt, unpublished). Interactions between plant genotypes in mixture cause the relationship between disease level and yield of a mixture to be highly complex and unpredictable (36). In contrast, yield stability seems to be strongly and more consistently associated with mixtures (15, 66, 106, 136, 153, 167, among others). Yield stability is often considered crucial in subsistence agriculture, and appropriately so. However, yield stability has also become crucial in industrialized agriculture, owing to the precarious economic situation facing commercial agriculture today. In fact, large, commercial growers in the United States are sometimes interested in mixtures more for their effect on yield stability than for yield level (66; C.C. Mundt, unpublished). Yield stability of mixtures could be due to disease control or compensation between host genotypes for damage caused by abiotic stresses such as cold injury (15, 36, 167), or other unknown genotype × environment interactions

(167, 169). Regardless of mechanism, it is usually impossible to predict at the time of planting which host genotype will yield best in a particular season. Given that some yield advantage is expected to growing mixtures, on average, a farmer will increase the chances of attaining high yield by sowing a mixture of high-performing cultivars (167, 169). It seems clear that a competitive mixture must usually consist of genotypes with high yield potential in pure stand (103, 136, 169).

Though more effort is required to produce seed of mixtures than is the case for single genotypes, there are several ways to provide mixed seed to farmers (103, 167). Multiline cultivars, which usually consist of several genotypes, are generally produced by a certifying agency, with lines being produced separately, bulked, and then provided to seed producers for increase and sale [see (4, 18)]. Seed of cultivar mixtures, which usually consist of a smaller number of genotypes, is usually mixed by commercial seedsmen or by growers themselves (94, 103). In Oregon, mixtures are commonly sold, even by the largest companies (103), and mixtures provide an attractive market niche for some seed producers (C.C. Mundt, unpublished). Some apprehension has been expressed regarding shifts of mixture components over time for small grain cultivar mixtures in some environments (167). In other localities, wheat cultivar mixtures are carried over for 3 to 4 years with few problems regarding component shifts (103).

Though mixture components must be compatible in terms of agronomic and quality characteristics, the difficulty of attaining such compatibility has often been overemphasized (36, 103, 167). For example, 13% and 18% of the Oregon (131) and Washington (164) winter wheat areas are currently being grown as cultivar mixtures, with no apparent agronomic or marketing difficulties. Further, there often is as much difference among plants or tillers of the same cultivar grown in the same field as there is between different cultivars in a mixture. Considerable height differences can often be accommodated by harvest machinery; occasionally, height differences even facilitate harvest (103). Height differences between cultivars that are too large, however, may necessitate processing more straw or stalk material than is desired (15, 103) and may require excessive attention by the operator to ensure that all of the crop is harvested. The importance of variation in crop maturity date will depend on the crop species and geographical location in question. In the Pacific Northwest region, where conditions become increasingly hot and dry as the wheat crop matures, large maturity differences at anthesis translate into very small difference at harvest. Thus, there is little problem in mixing wheat cultivars with different maturity (103), except at the highest elevations where cooler temperatures sometimes extend maturity differences. Compatibility for maturity date of field crop cultivars may be more critical in areas where summer rainfall is common, however [see (15)], and may be even more critical for some vegetable and fruit crops.

Differences in quality and marketing of mixtures will depend on the crop in question. For many field crops, the harvested product is often not segregated by cultivar upon sale, and environment can often have a greater influence on quality characteristics than does cultivar (103). Given that cultivar mixtures produce wheat

flour (36, 56, 103), wheat grain (145), barley malt (123, 155), barley grain (58), and rice grain (25) with quality equal to or better than the mean of its component cultivars in pure stand, there should usually be no difficulty involved with sale of mixtures containing genotypes that produce acceptable quality when grown alone. Indeed, mixtures can sometimes be used to improve the quality of a product (36, 56, 145). For crops that are sold to the consumer by cultivar (e.g., apples), it would be necessary to harvest the cultivars separately, sort by cultivar after harvest, or to develop multiline cultivars consisting of components with highly similar quality characteristics.

It is now uncommon for plant breeders to produce true pure-line cultivars of many field crops, and within-cultivar diversity may improve yield stability and reduce vulnerability to disease. For example, the most successful groundnut (*Arachis hypogea*) cultivars grown in the United States (e.g., 'Florigiant' and 'Florerunner') are mixtures developed by bulking phenotypically similar lines in the F_3 to F_5 generations (70). These cultivars have long dominated U.S. groundnut production, and have demonstrated a high level of stability over environments for yield and other characteristics (69). Interestingly, the soft white winter wheat cultivar Stephens was developed in a similar manner, but through the accidental bulking of lines early in the breeding process. Released in 1977, Stephens has been one of the most successful wheat cultivars in the United States, showing tremendous productivity and adaptability, and still comprised half of the Oregon winter wheat area in 2001 (131). Though largely anecdotal, such observations suggest that retaining diversity within cultivars may be highly beneficial in traditional breeding programs, and that diversity should be introduced into cultivars produced via biotechnology, for example, by transforming resistance genes into multiple host genetic backgrounds and by bulking phenotypically similar progeny resulting from a doubled haploid cross.

CONCLUSIONS

It is now 50 years since the pioneering call for use of multiline crop cultivars by Jensen (61). The usefulness of mixtures for control of powdery mildews and rusts of small grains, which account for the majority of mixture research, has been demonstrated repeatedly through experimental studies. There have been some major successes in using mixtures to control such diseases at a commercial scale. However, mixtures will be more useful under some epidemiological conditions than under others, and experimental methodology, especially scale issues, may be crucial in evaluating the potential usefulness of mixtures.

A data base is now accumulating to evaluate the effect of mixtures for other types of pathosystems. In the rare cases when all other variables can be held constant experimentally, and in mathematical models, it is possible to demonstrate that mixtures are, on average, less effective under some conditions, e.g., for crops with large plants. All else is rarely equal in the real world, however, and there are examples of mixtures providing both low and high degrees of disease control for

almost any type of pathosystem imaginable, including crops with large plants, and pathogens that demonstrate low host specificity, or are splash dispersed, soilborne, or insect vectored.

Despite the absence of strong evidence for rapid loss of mixture effectiveness owing to selection of complex pathogen genotypes, our knowledge in this area is inadequate. Empirical studies to address this issue are difficult to conduct, and mathematical models have taken a simplistic view by focusing mostly on static costs of virulence as the main mechanism countering selection for pathogen complexity in mixtures. Many other mechanisms that may potentially maintain pathogen diversity in mixtures need to be investigated. Studies of pathogen evolution need to consider both relative and absolute frequencies of pathogen genotypes, and mixtures should be managed to avoid strong selection for complex pathogen genotypes that are highly fit.

Theory and models have been useful in evaluating epidemic development and pathogen evolution in mixtures, especially when combined with results of empirical studies. However, current models do not describe events in the field accurately, and results from well-designed field experiments continue to limit our understanding of the effect of mixtures on disease development. Owing to host and pathogen complexity, field studies of mixtures are more difficult to conduct and more prone to error and bias than are many other types of field studies.

In the past, many agricultural researchers have assumed that mixtures will not provide adequate disease control, are impractical, or would prove to be unacceptable to farmers. These arguments are clearly invalid as generalities, and there are now many examples of mixtures contributing substantially to disease control, yield increases, and yield stability in commercial agriculture. On the other hand, the concept of functional diversity instructs that not all mixtures will provide benefits, and that use of mixtures will not be feasible in all cases. Multilines, cultivar mixtures, and other methods of genetic diversification should be considered as important tools for management of all crops, but must be appropriately evaluated within the context of the needs of the local agricultural industry and through direct interaction with farmers. Mixtures will not be the disease control tactic of choice in all cases. Given the need for a more sustainable agriculture based on models of natural ecosystems, however, host mixtures will likely play a much larger role in the next 50 years than they have in the past half century.

The *Annual Review of Phytopathology* is online at http://phyto.annualreviews.org

LITERATURE CITED

1. Ahmed HU, Finckh MR, Alfonso AF, Mundt CC. 1997. Epidemiological effect of gene deployment strategies on bacterial blight of rice. *Phytopathology* 87:66–70

2. Akanda SI, Mundt CC. 1996. Effects of two-component wheat cultivar mixtures on stripe rust severity. *Phytopathology* 86:347–53

3. Alexander HM, Roelfs AP, Cobbs G.

1986. Effects of disease and plant competition on yield in monocultures and mixtures of two wheat cultivars. *Plant Pathol.* 35:457–65

4. Allan RE, Line RF, Peterson CJ Jr, Rubenthaler GL, Morrison KJ, Rohde CR. 1983. Crew, a multiline wheat cultivar. *Crop Sci.* 23:1015–16

5. Assefa H, Van den Bosch F, Zadoks JC. 1995. Focus expansion of bean rust in cultivar mixtures. *Plant Pathol.* 44:503–9

6. Ayanru DKG, Browning JA. 1977. Effect of heterogeneous oat populations on the epiphytotic development of victoria blight. *New Phytol.* 79:613–23

7. Barrera JAS, Frederiksen RA. 1994. Evaluation of sorghum hybrid mixtures for controlling sorghum leaf-blight. *Plant Dis.* 78:499–503

8. Barrett JA. 1980. Pathogen evolution in multilines and variety mixtures. *Z. Pflanzenkr. Pflanzenschutz.* 87:383–96

9. Barrett JA. 1981. Disease progress curves and dispersal gradients in multilines. *Phytopathol. Z.* 100:361–96

10. Barrett JA, Wolfe MS. 1980. Pathogen response to host resistance and its implications in breeding programmes. *Eur. Mediterr. Plant Prot. Organ. Bull.* 10: 341–47

11. Berger RD, Bergamin A, Amorim L. 1997. Lesion expansion as an epidemic component. *Phytopathology* 87:1005–13

12. Blaise P, Gessler C. 1994. Cultivar mixtures in apple orchards as a means to control apple scab? In *Integrated Control of Pome Fruit Diseases*, ed. DJ Butt, pp. 105–12. *Norw. J. Agric. Sci. Suppl.* 17

13. Bonman JM, Khush GS, Nelson RJ. 1992. Breeding rice for resistance to pests. *Annu. Rev. Phytopathol.* 30:507–28

14. Boudreau MA, Mundt CC. 1997. Ecological approaches to disease control. In *Environmentally Safe Approaches to Crop Disease Control*, ed. J Rechcigl, N Rechcigl, pp. 33–62. Boca Raton, FL: CRC Press

15. Bowden R, Shroyer J, Roozeboom K, Claassen M, Evans P, et al. 2001. *Performance of Wheat Variety Blends in Kansas. Kansas State Univ. Agric. Ext. Bull.* 128 (www.oznet.ksu.edu/library/crpsl2/SRL128.pdf)

16. Brophy LS, Mundt CC. 1991. Influence of plant spatial patterns on disease dynamics, grain yield and plant competition in genetically diverse wheat populations. *Agric. Ecosyst. Environ.* 35:1–12

17. Browning JA, Frey KJ. 1969. Multiline cultivars as a means of disease control. *Annu. Rev. Phytopathol.* 14:355–82

18. Browning JA, Frey KJ. 1981. The multiline concept in theory and practice. See Ref. 60a, pp. 37–46

19. Buiel AAM, Verhaar MA, van den Bosch F, Hoogkamer W, Zadoks JC. 1989. Effect of cultivar mixtures on the wave velocity of expanding yellow rust foci in winter wheat. *Neth. J. Agric. Sci.* 37:75–78

20. Burdon JJ, Chilvers GA. 1977. Controlled environment experiments on epidemic rates of barley mildew in different mixtures of barley and wheat. *Oecologia* 28:141–46

21. Burdon JJ, Chilvers GA. 1982. Host density as a factor in disease ecology. *Annu. Rev. Phytopathol.* 20:143–66

22. Calonnec A, Goyeau H, de Vallavieille-Pope C. 1996. Effects of induced resistance on infection efficiency and sporulation of *Puccinia striiformis* on seedlings in varietal mixtures and on field epidemics in pure stands. *Eur. J. Plant Pathol.* 5:733–41

23. Castro A. 2001. *Cultivar Mixtures. The Plant Health Instructor*, DOI: 101094/PHI-A-2001-1230-01. St. Paul: Am. Phytopathol. Soc. (www.apsnet.org/education/AdvancedPlantPath/top.html)

24. Chakraborty S, Pettitt AN, Cameron DF, Irwin JAG, Davis RD. 1991. Anthracnose development in pure and mixed stands of the pasture legume *Stylosanthes-scabra*. *Phytopathology* 81:788–93

25. Chin KM, Husin AN. 1982. Rice variety mixtures. In *Proc. Padi Workshop,*

Bumbong Lima, Province Wellesley, Malaysia, pp. 203–16

26. Chin KM, Wolfe MS. 1984. Selection on *Erysiphe graminis* in pure and mixed stands of barley. *Plant Pathol.* 33:535–46

27. Chin KM, Wolfe MS. 1984. The spread of *Erysiphe graminis* f. sp. *hordei* in mixtures of barley varieties. *Plant Pathol.* 33:89–100

28. Cohan FM, King EC, Zawadzki P. 1994. Amelioration of the deleterious pleiotropic effects of an adaptive mutation in *Bacillus subtilis. Evolution* 48:81–95

29. Cournoyer BM. 1967. *Crown rust intensification within and dissemination from pureline and multiline oat varieties*. PhD thesis. Iowa State Univ., Ames

29a. Cowger C, Mundt CC. 2002. Effects of wheat cultivar mixtures on epidemic progression of Septoria tritici blotch and pathogenicity of *Mycosphaerella graminicola. Phytopathology* 92: In press

29b. Csada RD, James PC, Espie RHM. 1996. The "filedrawer problem" of nonsignificant results: Does it apply to biological research? *Oikos* 76:591–93

30. DiLeone JA, Mundt CC. 1994. Effect of wheat cultivar mixtures on populations of *Puccinia striiformis* races. *Plant Pathol.* 43:917–30

31. Dinoor A, Eshed N. 1984. The role and importance of pathogens in natural plant communities. *Annu. Rev. Phytopathol.* 22:443–66

32. Dubin HJ, Wolfe MS. 1994. Comparative behavior of three wheat cultivars and their mixture in India, Nepal, and Pakistan. *Field Crops Res.* 39:71–83

33. Elliot VJ, MacKenzie DR, Nelson RR. 1980. Effect of number of component lines on powdery mildew epidemics in a wheat multiline. *Phytopathology* 70:461–62 (Abstr.)

34. Ferrandino FJ. 1993. Dispersive epidemic waves: I. Focus expansion within a linear planting. *Phytopathology* 83:795–802

35. Finckh MR, Gacek ES, Czembor HJ, Wolfe MS. 1999. Host frequency and density effects on disease and yield in mixtures of barley. *Plant Pathol.* 48:807–16

36. Finckh MR, Gacek ES, Goyeau H, Lannou C, Merz U, et al. 2000. Cereal variety and species mixtures in practice. *Agronomie* 20:813–37

37. Finckh MR, Mundt CC. 1992. Plant competition and disease in genetically diverse wheat populations. *Oecologia* 91:81–92

38. Finckh MR, Mundt CC. 1992. Stripe rust, yield, and plant competition in wheat cultivar mixtures. *Phytopathology* 82:905–13

39. Finckh MR, Wolfe MS. 1997. The use of biodiversity to restrict plant diseases and some consequences for farmers and society. In *Ecology in Agriculture*, ed. LE Jackson, pp. 199–233. San Diego: Academic

40. Finckh MR, Wolfe MS. 1998. Diversification strategies. In *The Epidemiology of Plant Diseases*, ed. DG Jones, pp. 231–59. London: Chapman & Hall

41. Fitt BDL, McCartney HA. 1986. Spore dispersal in relation to epidemic models. In *Plant Disease Epidemiology*, Vol. 1, ed. KJ Leonard, WE Fry, pp. 311–45. New York: MacMillan

42. Fitt BDL, McCartney HA, Walklate PJ. 1989. The role of rain in dispersal of pathogen inoculum. *Annu. Rev. Phytopathol.* 27:241–70

43. Fleming RA. 1983. Development of a simple mechanistic model of cereal rust progress. *Phytopathology* 73:308–12

44. Francis CA, ed. 1986. *Multiple Cropping Systems*. New York: MacMillan

45. Garrett KA, Mundt CC. 1999. Epidemiology in mixed host populations. *Phytopathology* 89:984–90

46. Garrett KA, Mundt CC. 2000. Effects of planting density and the composition of wheat cultivar mixtures on stripe rust: an analysis taking into account limits to the replication of controls. *Phytopathology* 90:1313–21

47. Garrett KA, Mundt CC. 2000. Host diversity can reduce potato late blight severity

for focal and general patterns of primary inoculum. *Phytopathology* 90:1307–12

48. Garrett KA, Nelson RJ, Mundt CC, Chacon G, Jaramillo RE, Forbes GA. 2001. The effects of host diversity and other management components on epidemics of potato late blight in the humid highland tropics. *Phytopathology* 91:993–1000

49. Gieffers W, Hesselbach J. 1988. Disease incidence and yield of different cereal cultivars in pure stands and mixtures. I. Spring barley (*Hordeum vulgare* L.). *Z. Pflanzenkrankh. Pflanzenschutz* 95:46–62

50. Gieffers W, Hesselbach J. 1988. Disease incidence and yield of different cereal cultivars in pure stands and mixtures. II. Winter barley (*Hordeum vulgare* L.). *Z. Pflanzenkrankh. Pflanzenschutz* 95:63–69

51. Goleniewski G, Newton AC. 1994. Modelling the spread of fungal diseases using a nearest neighbor approach. *Plant Pathol.* 43:631–43

52. Gumpert FM. 1989. Measuring disease progress in pure and mixed stands of plant cultivars. *Phytopathology* 79:968–73

53. Halloin JM, Johnson DJ. 2000. Reduction of sugarbeet losses from Rhizoctonia crown and root rot by use of mixtures of resistant and susceptible varieties. *Phytopathology* 90:S33 (Abstr.)

54. Hariri D, Fouchard M, Prud'homme H. 2001. Incidence of *Soil-borne wheat mosaic virus* in mixtures of susceptible and resistant wheat cultivars. *Eur. J. Plant Pathol.* 107:625–31

55. Huang R, Kranz J, Welz HG. 1994. Selection of pathotypes of *Erysiphe graminis* f. sp. *hordei* in pure and mixed stands of spring barley. *Plant Pathol.* 43:458–70

56. Jackson LF, Wennig RW. 1997. Use of wheat cultivar blends to improve grain yield and quality and reduce disease and lodging. *Field Crops Res.* 52:261–69

57. James WC, Shih CS, Callbeck LC, Hodgson WA. 1973. Interplot interference in field experiments with late blight of potato (*Phytophthora infestans*). *Phytopathology* 63:1269–75

58. Jedel PE, Helm JH, Burnett PA. 1998. Yield, quality and stress tolerance of barley mixtures in central Alberta. *Can. J. Plant Sci.* 78:429–36

59. Jeger MJ, Griffiths E, Jones DG. 1981. Disease progress of non-specialised fungal pathogens in intraspecific mixed stands of cereal cultivars. I. Models. *Ann. Appl. Biol.* 98:187–98

60. Jeger MJ, Jones DG, Griffiths E. 1981. Disease progress of non-specialised fungal pathogens in intraspecific mixed stands of cereal cultivars. II. Field experiments. *Ann. Appl. Biol.* 98:199–210

60a. Jenkyn JF, Plumb RT, eds. 1981. *Strategies for the Control of Cereal Disease.* Oxford: Blackwell

61. Jensen NF. 1952. Intra-varietal diversification in oat breeding. *Agron. J.* 44:50–54

62. Kardin MK, Groth JV. 1989. Density-dependent fitness interactions in the bean rust fungus. *Phytopathology* 79:409–12

63. Karjalainen R. 1986. Spring wheat mixtures in northern crop production: ability of mixtures to buffer disease development and yield loss caused by *Septoria nodorum*. *J. Agric. Sci. Finland* 58:33–42

64. Karjalainen R, Peltonen-Sainio P. 1993. Effect of oat cultivar mixtures on disease progress and yield reduction caused by barley yellow dwarf virus. *Z. Pflanzenkrankh. Pflanzenschutz* 100:58–68

65. Katsuya K, Green GJ. 1967. Reproductive potentials of races 15B and 56 of wheat stem rust. *Can. J. Bot.* 45:1077–91

66. Kessler K. 1997. Wheat blends stabilize yields. *Furrow*, Jan., pp. 27–28

67. Kiyosawa S. 1989. Breakdown of blast resistance in relation to general strategies of resistance gene deployment to prolong effectiveness of resistance in plants. In *Plant Disease Epidemiology*, Vol. 2, ed. KJ Leonard, WE Fry, pp. 251–83. New York: McGraw-Hill

68. Kiyosawa S, Shiyomi M. 1972. A theoretical evaluation of the effect of mixing resistant variety with susceptible variety

for controlling plant diseases. *Ann. Phytopathol. Soc. Jpn.* 38:41–51

69. Knauft DA, Gorbet DW. 1991. Agronomic performance and genetic shifts of genotype mixtures in peanut. *Euphytica* 52:85–90

70. Knauft DA, Norden AJ, Gorbet DW. 1987. Peanut. In *Principles of Cultivar Development*, ed. WR Fehr, pp. 346–84. New York: MacMillan

71. Knott EA, Mundt CC. 1990. Combining ability analysis of wheat cultivar mixtures under diseased and non-diseased conditions. *Theor. Appl. Genet.* 80:313–20

72. Koizumi S. 2001. Rice blast control with multilines in Japan. See Ref. 94a, pp. 143–57

73. Koizumi S, Kato H. 1987. Effect of mixed plantings of susceptible and resistant rice cultivars on leaf blast development. *Ann. Phytopathol. Soc. Jpn.* 53:28–38

74. Kolmer JA. 1995. Selection of *Puccinia recondita* f.sp. *tritici* virulence phenotypes in three multilines of Thatcher wheat lines near isogenic for leaf rust resistance genes. *Can. J. Bot.* 73:1081–88

75. Kousik CS, Sanders DC, Ritchie DF. 1996. Mixed genotypes combined with copper sprays to manage bacterial spot of bell peppers. *Phytopathology* 86:502–8

76. Lannou C. 2001. Intra-pathotype diversity for aggressiveness and pathogen evolution in cultivar mixtures. *Phytopathology* 91:500–10

77. Lannou C, de Vallavieille-Pope C, Biass C, Goyeau H. 1994. The efficacy of mixtures of susceptible and resistant hosts to two wheat rusts with different lesion size: controlled condition experiments and computer simulations. *J. Phytopathol.* 140:227–37

78. Lannou C, de Vallavieille-Pope C, Goyeau H. 1994. Host mixture efficacy in disease control: effects of lesion growth analyzed through computer-simulated epidemics. *Plant Pathol.* 43:651–62

79. Lannou C, de Vallavieille-Pope C, Goyeau H. 1995. Induced resistance in host mixtures and its effect on disease control in computer-simulated epidemics. *Plant Pathol.* 44:478–89

80. Lannou C, Mundt CC. 1996. Evolution of a pathogen population in host mixtures. I. Study of the simple race-complex race equilibrium. *Plant Pathol.* 45:440–53

81. Lannou C, Mundt CC. 1997. Evolution of a pathogen population in host mixtures: rate of emergence of complex races. *Theor. Appl. Genet.* 94:991–99

82. Leach JE, Vera Cruz CM, Bai J, Leung H. 2001. Pathogen fitness penalty as a predictor of durability of disease resistance genes. *Annu. Rev. Phytopathol.* 39:187–224

83. Leonard KJ. 1969. Factors affecting rates of stem rust increase in mixed plantings of susceptible and resistant oat varieties. *Phytopathology* 59:1845–50

84. Leonard KJ, Czochor RJ. 1980. Theory of genetic interactions among populations of plants and their pathogens. *Annu. Rev. Phytopathol.* 18:237–58

85. Levin BR, Veronique P, Walker N. 2000. Compensatory mutations, antibiotic resistance and the population genetics of adaptive evolution in bacteria. *Genetics* 154:985–97

86. Lopez CG, Mundt CC. 2000. Using mixing ability analysis from two-way cultivar mixtures to predict the performance of cultivars in complex mixtures. *Field Crops Res.* 68:121–32

87. Luthra JK, Rao MV. 1979. Escape mechanism operating in multilines and its significance in relation to leaf rust epidemics. *Indian J. Genet. Plant Breed.* 39:38–49

88. Luthra JK, Rao MV. 1979. Multiline cultivars—how their resistance influences leaf rust epidemics in wheat. *Euphytica* 28:137–44

89. MacHardy WE, Gadoury DM, Gessler C. 2001. Parasitic and biological fitness of *Venturia inequalis*: relationship to disease management strategies. *Plant Dis.* 85:1036–51

90. Madden LV. 1992. Rainfall and the dispersal of fungal spores. *Adv. Plant Pathol.* 8:39–79

91. Marshall DR. 1989. Modeling the effects of multiline varieties on the population genetics of plant pathogens. In *Plant Disease Epidemiology*, Vol. 2, ed. KJ Leonard, WE Fry, pp. 284–317. New York: McGraw-Hill

92. McCracken AR, Dawson WM. 1998. Short rotation coppice willow in Northern Ireland since 1973: development of the use of mixtures in the control of foliar rust (*Melampsora* spp.). *Eur. J. For. Pathol.* 28:241–50

93. McDonald BA, Allard RW, Webster RK. 1988. Responses of two-, three-, and four-component barley mixtures to a variable pathogen population. *Crop Sci.* 28:447–52

94. Merz U, Valenghi D. 1997. 'Extenso' production and cereal mixtures in Switzerland. In *Variety Mixtures in Theory and Practice*, ed. MS Wolfe, pp. 9–10. Grignon, France: COST Action 817 (www.scri.sari.ac.uk/TiPP)

94a. Mew TW, Borromeo E, Hardy B, eds. 2001. *Exploiting Biodiversity for Sustainable Pest Management, Proc. Impact Symp. Exploit. Biodivers. Sustain. Pest Manag., Kunming, China*, 21–23, Aug. 2000. Los Baños, Philippines: Int. Rice Res. Inst.

95. Milgroom MG. 1990. A stochastic model for the initial occurrence and development of fungicide resistance in plant pathogen populations. *Phytopathology* 80:410–16

96. Minogue KP, Fry WE. 1983. Models for the spread of disease: model description. *Phytopathology* 73:1168–73

97. Miot S, Frey P, Pinon J. 1999. Varietal mixture of poplar clones: effect on infection by *Melampsora larici-populina* and on plant growth. *Eur. J. For. Pathol.* 29:411–23

98. Moreno-Ruiz G, Castillo-Zapata J. 1990. The variety Colombia: a variety of coffee with resistance to rust (*Hemileia vastatrix* Berk & Br). *Cent. Nac. Invest. Cafe, Cenicafe, Chinchina-Caldas, Colombia. Tech. Bull.* 9

99. Morrell V. 1997. Antibiotic resistance: road of no return. *Science* 278:575–76

100. Muller K, McDermott JM, Wolfe MS, Limpert E. 1996. Analysis of diversity in populations of plant pathogens: the barley powdery mildew pathogen across Europe. *Eur. J. Plant Pathol.* 102:385–95

101. Mundt CC. 1990. Disease dynamics in agroecosystems. In *Agroecology*, ed. CR Carroll, JH Vandermeer, PM Rossett, pp. 263–69. New York: McGraw-Hill

102. Mundt CC. 1994. Techniques to manage pathogen co-evolution with host plants to prolong resistance. In *Rice Pest Science and Management*, ed. PS Teng, KL Heong, K Moody, pp. 193–205. Los Baños, Philippines: Int. Rice Res. Inst.

103. Mundt CC. 1994. Use of host genetic diversity to control cereal diseases: implications for rice blast. In *Rice Blast Disease*, ed. S Leong, RS Zeigler, PS Teng, pp. 293–307. Cambridge: CABI Int.

104. Mundt CC. 1997. Disease increase in host mixtures. In *Exercises in Plant Disease Epidemiology*, ed. L Francl, D Nehr, pp. 119–22. St. Paul: APS Press

105. Mundt CC. 2001. Varietal diversification and disease control. See Ref. 94a, pp. 135–42

106. Mundt CC. 2002. Performance of wheat cultivars and cultivar mixtures in the presence of *Cephalosporium* stripe. *Crop Prot.* In press

107. Mundt CC, Brophy LS. 1988. Influence of number of host genotype units on the effectiveness of host mixtures for disease control: a modeling approach. *Phytopathology* 78:1087–94

108. Mundt CC, Brophy LS, Kolar SC. 1996. Effect of genotype unit number and spatial arrangement on severity of yellow rust in wheat cultivar mixtures. *Plant Pathol.* 45:215–22

109. Mundt CC, Brophy LS, Schmitt ME.

1995. Choosing crop cultivars and mixtures under high versus low disease pressure: a case study with wheat. *Crop Prot.* 14:509–15

110. Mundt CC, Brophy LS, Schmitt ME. 1995. Disease severity and yield of pure-line wheat cultivars and mixtures in the presence of eyespot, yellow rust, and their combination. *Plant Pathol.* 44:173–82

111. Mundt CC, Browning JA. 1985. Development of crown rust epidemics in genetically diverse oat populations: effect of genotype unit area. *Phytopathology* 75:607–10

112. Mundt CC, Browning JA. 1985. Genetic diversity and cereal rust management. In *The Cereal Rusts*, Vol. 2, ed. AP Roelfs, WR Bushnell. Orlando: Academic

113. Mundt CC, Cowger C, Garrett KA. 2002. Relevance of integrated management to resistance durability. *Euphytica.* In press

114. Mundt CC, Cowger C, Hoffer ME. 1999. Disease management using variety mixtures. In *Septoria and Stagonospora Diseases of Cereals: A Compilation of Global Research*, ed. M van Ginkel, A McNab, J Krupinsky, pp. 111–16. Mexico, DF: CIMMYT

115. Mundt CC, Hayes PM, Schön CC. 1994. Influence of variety mixtures on severity of scald and net blotch and on the yield of barley. *Plant Pathol.* 43:356–61

116. Mundt CC, Karow RS. 1995. How does disease affect club wheat performance? *Oregon Wheat*, July, pp. 12–13

117. Mundt CC, Leonard KJ. 1985. Effect of host genotype unit area on epidemic development of crown rust following focal and general inoculations of mixtures of immune and susceptible oat plants. *Phytopathology* 75:1141–45

118. Mundt CC, Leonard KJ. 1986. Analysis of factors affecting disease increase and spread in mixtures of immune and susceptible plants in computer-simulated epidemics. *Phytopathology* 76:832–40

119. Mundt CC, Leonard KJ. 1986. Effect of host genotype unit area on development of focal epidemics of bean rust and common maize rust in mixtures of resistant and susceptible plants. *Phytopathology* 76:895–900

120. Mundt CC, Leonard KJ, Thal WM, Fulton JH. 1986. Computerized simulation of crown rust epidemics in mixtures of immune and susceptible oat plants with different genotype unit areas and spatial distributions of initial disease. *Phytopathology* 86:590–98

121. Munk L. 1983. Response of a powdery mildew population to a barley variety mixture. In *Durable Resistance in Crops*, ed. F Lamberti, JM Waller, NA Van der Graaf, pp. 105–7. New York: Plenum

122. Newton AC, Ellis RP, Hackett CA, Guy DC. 1997. The effect of component number on *Rhynchosporium secalis* infection and yield in mixtures of winter barley cultivars. *Plant Pathol.* 45:930–38

123. Newton AC, Swanston JS, Guy DC, Ellis RP. 1998. The effect of cultivar mixtures on malting quality in winter wheat. *J. Ind. Brew.* 104:41–51

124. Newton AC, Thomas WTB. 1992. The effect of specific and non-specific resistance in mixtures of barley genotypes on infection by mildew (*Erysiphe graminis* f. sp. *hordei*) and on yield. *Euphytica* 59:73–81

125. Newton AC, Thomas WTB. 1993. The interaction of either an effective or a defeated major gene with non-specific resistance on mildew infection (*Erysiphe graminis* f. sp. *hordei*) and yield in mixtures of barley. *J. Phytopathol.* 139:268–74

126. Newton MR, Kinkel LL, Leonard KJ. 1997. Competition and density-dependent fitness in a plant parasitic fungus. *Ecology* 78:1774–84

127. Newton MR, Kinkel LL, Leonard KJ. 1998. Determinants of density- and frequency-dependent fitness in competing plant pathogens. *Phytopathology* 88:45–51

128. Ntahimpera N, Dillard HR, Cobb AC, Seem RC. 1996. Colletotrichum development in mixtures of resistant and susceptible dry bean cultivars. *Phytopathology* 86:668–73

129. Nugugi HK, King SB, Holt J, Julian AM. 2001. Simultaneous temporal progress of sorghum anthracnose and leaf blight in crop mixtures with disparate patterns. *Phytopathology* 91:720–29

130. Ohara RB, Brown JKM. 1996. Frequency- and density-dependent selection in wheat powdery mildew. *Heredity* 77:439–47

131. Oregon Agric. Stat. Serv. 2000. *1999– 2000 Oregon Agriculture & Fisheries Statistics*. Salem, OR: Oregon Dep. Agric.

132. Ostergaard H. 1983. Predicting development of epidemics on cultivar mixtures. *Phytopathology* 73:166–72

133. Parlevliet JE. 1981. Stabilizing selection in crop patho-systems: an empty concept or a reality? *Euphytica* 30:259–69

134. Parlevliet JE, van Ommeren A. 1975. Partial resistance of barley to leaf rust, *Puccinia hordei*. II. Relationship between field trials, micro plot tests and latent period. *Euphytica* 24:293–303

135. Paysour RE, Fry WE. 1983. Interplot interference: a model for planning field experiments with aerially disseminated pathogens. *Phytopathology* 73:1014–20

136. Pfahler PL, Linskens HF. 1979. Yield stability and population diversity in oats (*Avena* sp.). *Theor. Appl. Genet.* 54:1–5

137. Pfleeger TG, Mundt CC. 1998. Wheat leaf rust severity as affected by plant density and species proportion in simple communities of wheat and wild oats. *Phytopathology* 88:708–14

138. Pielou EC. 1977. *Mathematical Ecology*. New York: Wiley

139. Power AG. 1987. Plant community diversity, herbivore movement, and an insect-transmitted disease of maize. *Ecology* 68:1658–69

140. Power AG. 1990. Cropping systems, insect movement, and the spread of insect-transmitted diseases in crops. In *Agroecology*, ed. SR Gliessman, pp. 47–69. New York: Springer-Verlag

141. Power AG. 1991. Virus spread and vector dynamics in genetically diverse plant populations. *Ecology* 72:232–41

142. Priestly RH. 1981. Choice and deployment of resistant cultivars for cereal rust control. See Ref. 60a, pp. 65–72

143. Priestly RH, Bayles R. 1982. Varietal diversification as a means of reducing the spread of cereal diseases in the United Kingdom. *J. Natl. Inst. Agric. Bot.* 15:205–14

144. Robinson RA. 1976. *Plant Pathosystems*. New York: Springer-Verlag

145. Sarandon SJ, Sarandon R. 1995. Mixture of cultivars: pilot field trial of an ecological alternative to improve production or quality of wheat (*Triticum aestivum*). *J. Appl. Ecol.* 32:288–94

146. Saur L, Mille B. 1997. Disease progress of *Pseudocercosporella herpotrichoides* in mixed stands of winter wheat cultivars. *Agronomie* 17:113–18

147. Schmidt RA. 1978. Diseases in forest ecosystems: the importance of functional diversity. In *Plant Disease: An Advanced Treatise*, Vol. 2, ed. JG Horsfall, EB Cowling, pp. 287–315. New York: Academic

148. Segal A, Browning JA, Fishbeck G, Wahl I. 1982. Balance in indigenous plant populations. In *Resistance to Diseases and Pests in Forest Trees*, ed. HM Heybroek, BR Stephan, K von Weissenberg, pp. 361– 70. Wageningen: PUDOC

149. Segal A, Manisterski J, Fishbeck G, Wahl I. 1980. How plant populations defend themselves in natural ecosystems. In *Plant Disease: An Advanced Treatise*, Vol. 5, ed. JG Horsfall, EB Cowling, pp. 75– 102. New York: Academic

150. Sharma RC, Dubin HJ. 1996. Effect of wheat cultivar mixtures on spot blotch (*Bipolaris sorokiniana*). *Field Crops Res.* 48:95–101

151. Shaw MW, Ostergard H. 1998. Further comments on models of pathogen co-evolution in cultivar mixtures and the

definition of pathogenic fitness. *Phytopathology* 88:492–93

152. Sitch L, Whittington WJ. 1983. The effect of variety mixtures on the development of swede powdery mildew. *Plant Pathol.* 32:41–46

153. Smithson JB, Lenne JM. 1996. Varietal mixtures: a viable strategy for sustainable productivity in subsistence agriculture. *Ann. Appl. Biol.* 128:127–58

154. Sun P, Yang XB. 1999. Two properties of a gene-for-gene coevolution system under human perturbations. *Phytopathology* 89:811–16

155. Swanston JS, Newton AC, Guy DC, Gacek ES. 2000. Malting performance of barley cultivar mixtures from the UK and Poland. *J. Ind. Brew.* 106:239–43

156. Tapsoda H, Wilson JP. 1999. Increasing complexity of resistance in host populations through intermating to manage rust of pearl millet. *Phytopathology* 89:450–55

157. Thurston HD. 1992. *Sustainable Practices for Plant Disease Management in Traditional Farming Systems.* Boulder, CO: Westview

158. Van den Bosch F, Frinking F, Metz JAJ, Zadoks JC. 1990. Focus expansion in plant disease. IV. Expansion rates in mixtures of resistant and susceptible hosts. *Phytopathology* 80:598–602

159. van den Bosch F, Zadoks JC, Metz JAJ. 1988. Focus expansion in plant disease. I: The constant rate of focus expansion. *Phytopathology* 78:54–58

160. van den Bosch F, Zadoks JC, Metz JAJ. 1988. Focus expansion in plant disease. II. Realistic parameter-sparse models. *Phytopathology* 78:59–64

161. Vanderplank JE. 1963. *Plant Diseases: Epidemics and Control.* New York: Academic

162. Vera Cruz CM, Bai J, Ona I, Leung H, Nelson RJ, et al. 2000. Predicting durability of a disease resistance gene based on an assessment of the fitness loss and epidemiological consequences of avirulence gene mutation. *Proc. Natl. Acad. Sci. USA* 97:13500–5

163. Villareal LMMA, Lannou C. 2000. Selection for increased spore efficacy by host genetic background in a wheat powdery mildew population. *Phytopathology* 90:1300–6

164. Washington Agric. Stat. Serv. 2000. *Washington Agricultural Statistics 2000.* Olympia, WA: Wash. State Dep. Agric.

165. Wilcox JR, St. Martin SK. 1998. Soybean genotypes resistant to *Phytophthora sojae* and compensation for yield losses of susceptible isolines. *Plant Dis.* 82:303–6

166. Wilson JP, Gates RN, Panwar MS. 2001. Dynamic multiline population approach to resistance gene management. *Phytopathology* 91:255–60

167. Wolfe MS. 1985. The current status and prospects of multiline cultivars and variety mixtures for disease resistance. *Annu. Rev. Phytopathol.* 23:251–73

168. Wolfe MS. 1992. Maintaining the value of our varieties. In *Barley Genetics VI*, Vol. 2, ed. L Munk, pp. 1055–67. Copenhagen: Munksgaard Int. Publ.

169. Wolfe MS, Barrett JA. 1980. Can we lead the pathogen astray? *Plant Dis.* 64:148–55

170. Wolfe MS, Barrett JA, Jenkins JEE. 1981. The use of cultivar mixtures for disease control. See Ref. 60a, pp. 73–80

171. Wolfe MS, Brandle U, Koller B, Limpert E, McDermott JM, et al. 1992. Barley mildew in Europe: population biology and host resistance. *Euphytica* 63:125–39

172. Wolfe MS, McDermott JM. 1994. Population genetics of plant pathogen interactions: the example of the *Erysiphe graminis-Hordeum vulgare* pathosystem. *Annu. Rev. Phytopathol.* 32:89–113

173. Wolfe MS, Schwarzbach E. 1978. Patterns of race changes in powdery mildews. *Annu. Rev. Phytopathol.* 16:159–80

174. Xu X-M, Ridout MS. 2000. Stochastic simulation of the spread of race-specific and race-nonspecific aerial fungal

pathogens in cultivar mixtures. *Plant Pathol.* 49:207–18

175. Yang XB, Ferrandino FJ. 1998. Linear models to estimate relative parasitic fitness: a reply. *Phytopathology* 88:490–91

176. Yong L, Zadoks JC. 1992. A decision model for variety mixtures to control yellow rust on winter wheat. *Agric. Syst.* 38:17–33

177. Zeigler RS, Cuoc LX, Scott RP, Bernardo MA, Chen DH, et al. 1995. The relationship between lineage and virulence in *Pyricularia oryzae* in the Philippines. *Phytopathology* 85:443–51

178. Zhu Y, Chen H, Fan J, Wang Y, Li Y, et al. 2000. Genetic diversity and disease control in rice. *Nature* 406:718–22

Contents

ERRATA
   An online log of corrections to *Annual Review of Phytopathology* chapters
   (if any, 1997 to the present) may be found at http://phyto.annualreviews.org/